

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 453.

Location/Qualifiers

FEATURES

source

1..595  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:604040"  
/tissue\_type="Purified pancreatic islet"  
/lab\_host="DH10B"  
/clone\_lib="HR85 islet"  
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size-selected on agarose gel. Average insert size ~1kb. 5'  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

SE COUNT

IGIN

Query Match 35.2%; Score 591.0; DB 13; Length 595;  
Best Local Similarity 99.7%; Pred. No. 3.9e-132;  
Matches 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

635 AGAAGGAAGCAAGACCTCCAAATGTTCAAGGAGAGATTGAACAAATGGCCCTCCCC 694  
1 AGAAGGAAGCAAGACCTCCAAATGTTCAAGGAGAGATTGAACAAATGGCCCTCCCC 60  
695 AACTGTTATCCCATTTACCTTTTCCTCCACCGAGTCTATTTCAAGACATATCCAGTGGAA 754  
61 AACTGTTATCCCATTTACCTTTTCCTCCACCGAGTCTATTTCAAGACATATCCAGTGGAA 120  
755 TAACAGTATATGTTCTGTTTACAGATGTTGTTTACTGTTAGGAGATGTTATTTT 814  
121 TAACAGTATATGTTCTGTTTACAGATGTTGTTTACTGTTAGGAGATGTTATTTT 180  
815 TAAGTTACCATATTAAGTGTGTAATAAAGGGGACAGAGAGAAATCTATAAAGGC 874  
181 TAAGTTACCATATTAAGTGTGTAATAAAGGGGACAGAGAGAAATCTATAAAGGC 240  
875 CATGTTACATGCTATGAACTTTGTTGTTTCTGTTATTAATGTTACATTTATTAGG 934  
241 CATGTTACATGCTATGAACTTTGTTGTTTCTGTTATTAATGTTACATTTATTAGG 300  
935 AGTGGGTTTCGTTGGGTTAGGTGATAAATAATAGGATCATTTGAAGAAATTTGAAGAAC 994  
301 AGTGGGTTTCGTTGGGTTAGGTGATAAATAATAGGATCATTTGAAGAAATTTGAAGAAC 360  
995 TAGGATCATGAGAGAAACTGTTTCTTACCTGAAATTTAACTATGAAACACACTTAAC 1054  
361 TAGGATCATGAGAGAAACTGTTTCTTACCTGAAATTTAACTATGAAACACACTTAAC 420  
1055 AATCTTACAGGTTTCTAGATATTAAGTGAATATTAATCTCCGTCCTGAGGTTAGTGTG 1114  
421 AATCTTACAGGTTTCTAGATATTAAGTGAATATTAATCTCCGTCCTGAGGTTAGTGTG 480  
1115 ATCTTTGACTCTGTAATTTATTTTGAATTTCTATCAGTGTATTTATGACACTGGCCTC 1174  
481 ATCTTTGACTCTGTAATTTATTTTGAATTTCTATCAGTGTATTTATGACACTGGCCTC 540  
1175 CTGCGAGATCTTCTAGAGACCACTTAATGCAAGGCTGACAGAGAAACCTCTTTC 1229  
541 CTGCGAGATCTTCTAGAGACCACTTAATGCAAGGCTGACAGAGAAACCTCTTTC 595

## RESULT 2

AL138780/c

LOCUS

DEFINITION

3' similar to TR:Q92772 P56 KINASE PROTEIN KINASE. ; mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL138780  
AL138780.1 GI:3644752  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 499)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 279 Std Error: 0.00  
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High quality sequence stop: 393.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1737958"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pTT3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAAGTGGAGCGCCGCCCAATTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pTT3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 140 a 102 c 91 g 166 t

ORIGIN

Query Match

Best Local Similarity

Matches 475; Conservative

28.2%; Score 475; DB 9; Length 499;

Pred. No. 6.7e-104;

Mismatches 0; Indels 0; Gaps 0;

QY 420 GTATCAGGACCTCCCTGTTCAGATCATTCAGGGCTGATTTGCTTCAATGGAAACACAG 479

Db 499 GTATCAGGACCTCCCTGTTCAGATCATTCAGGGCTGATTTGCTTCAATGGAAACACAG 440

QY 480 CACTGAGAACCAATTTGGTTCTGAACCTGATGATCTTGCACCTTGATGATGATCTTTC 539

Db 439 CACTGAGAACCAATTTGGTTCTGAACCTGATGATCTTGCACCTTGATGATGATCTTTC 380

QY 540 TTGCACCAAGAGTGTGATATCCCAAGAGGAGAGATTCATGTTTGTGATCTTCTTCT 599

Db 379 TTGCACCAAGAGTGTGATATCCCAAGAGGAGAGATTCATGTTTGTGATCTTCTTCT 320

QY 600 GAATCCCTGCAATTTCTGAGGAAGCCCTTTAGAAAGAGGAAAGAAAGAAAGAAAGAAAG 659

Db 319 GAATCCCTGCAATTTCTGAGGAAGCCCTTTAGAAAGAGGAAAGAAAGAAAGAAAGAAAG 260

QY 660 TGTTCACAGAGAGATTGAACAAATGGCCCTCCCAACTGTTATCCCAATACCTTTCAAG 719  
 Db 259 TGTTTCAAGAGAGATTGAACAAATGGCCCTCCCAACTGTTATCCCAATACCTTTCAAG 200  
 QY 720 TCCACCGAGCTATTTCAAGACATATCCAGTGGAAATCAAGTATAGTGGTCTTGTATCA 779  
 Db 199 TCCACCGAGCTATTTCAAGACATATCCAGTGGAAATCAAGTATAGTGGTCTTGTATCA 140  
 QY 780 TGAATGCTATTTACTGTTAGGAGATTGTATATTTTAAGTTACCATGATTAAGTGTGT 839  
 Db 139 TGAATGCTATTTACTGTTAGGAGATTGTATATTTTAAGTTACCATGATTAAGTGTGT 80  
 QY 840 AAAAAAGGGGACAGAGAGAAATTAATAAAGGCCATGTTACTCATGCAATTCGAA 894  
 Db 79 AAAAAAGGGGACAGAGAGAAATTAATAAAGGCCATGTTACTCATGCAATTCGAA 25

RESULT 3  
 BM272057/c.  
 LOCUS  
 DEFINITION  
 Q97TKO SER/THR KINASE KIAHRE.1; mRNA sequence.  
 BM272057  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 AUTHORS  
 Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kestner, K.,  
 Lemshka, I., Scarce, M., Brestelli, J., Gradwohl, J., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,  
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas  
 , M., Gibbons, M., McCann, R., Cole, R., Tsagaris, W., Williams, T.,  
 Jackson, Y. and Bowers, Y.

TITLE  
 JOURNAL  
 COMMENT  
 Other ESTs: ig38e04.x1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohpc.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 186.  
 Location/Qualifiers  
 1. 621

FEATURES  
 source  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_lib="HR85 islet"  
 /notes="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming. ~1kb. 5'  
 Size selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."  
 163 a 120 c 123 g 215 t

ORIGIN

Query Match 28.1%; Score 472.6; DB 12; Length 621;  
 Best Local Similarity 86.1%; Pred. No. 2.7e-103;  
 Matches 574; Conservative 0; Mismatches 4; Indels 89; Gaps 1;  
 QY 219 AGTAAGAAAAGAGAAATATCTCCAGGACAGATGTCGGTTGCTGCACTAAACTATAT 278  
 Db 621 AGTAAGAAAAGAGAAATATCTCCAGGACAGATGTCGGTTGCTGCACTAAACTATAT 562  
 QY 279 CATCTCCCTGAACCTAAGAGACATCTGGAGGACATAGCTCGAAATTCAGAGCTAAACAGAAA 338  
 Db 561 CATCTCCCTGAACCTAAGAGACATCTGGAGGACATAGCTCGAAATTCAGAGCTAAACAGAAA 502  
 QY 339 GAGAGCAAAATCTTTTTCAGAAATCTCGAAATTCCTTCTGCTGCTGCTATGCTGCAAC 398  
 Db 501 GAGAGCAAAATCTTTTTCAGAAATCTCGAAATTCCTTCTGCTGCTGCTATGCTGCAAC 442  
 QY 399 CCAGTATTATCATCATCATCAGGTATCAGGACCTCCCTCTGCAGATGATTCCAGGGGCTGAT 458  
 Db 441 CCAGTATTATCATCATCATCAGGTATCAGGACCTCCCTCTGCAGATGATTCCAGGGGCTGAT 422  
 QY 459 TTGCTCTCAAAATGGAACACAGCACTGAGAACCAATTTTGGTCTGCACTGATGATGCTCT 518  
 Db 421 TTGCTCTCAAAATGGAACACAGCACTGAGAACCAATTTTGGTCTGCACTGATGATGCTCT 411  
 QY 519 TGCACCTTTCAGATGACATCTTTCTTCAGCAAGAGATCTGATATCCCAAGAGAGAGATCA 578  
 Db 410 TGCACCTTTCAGATGACATCTTTCTTCAGCAAGAGATCTGATATCCCAAGAGAGAGATCA 351  
 QY 579 TGGTTTTCAGATGATTTCTTCTGCACTGCTGCACTTTTCTGAGGAGGCTCTTAGAGAA 638  
 Db 350 TGGTTTTCAGATGATTTCTTCTGCACTGCTGCACTTTTCTGAGGAGGCTCTTAGAGAA 291  
 QY 639 GGAAGACAAAGACCTCCAAATGTTTCAAGGAGAGATGAAACAATGCTCCCTCCCAACT 698  
 Db 290 GGAAGACAAAGACCTCCAAATGTTTCAAGGAGAGATGAAACAATGCTCCCTCCCAACT 231  
 QY 699 GTTATCCCATTCACCTTTTCAGCTCCAGATGCTATTTTCAAGACATATCCCAAGGATCA 758  
 Db 230 GTTATCCCATTCACCTTTTCAGCTCCAGATGCTATTTTCAAGACATATCCCAAGGATCA 171  
 QY 759 AGTATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818  
 Db 170 AGTATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111  
 QY 819 TTACCATGATTAAAGTGTGTAAAGAGGGGGACAGAGAAATATCTATAAAGGCCATG 878  
 Db 110 TTACCATGATTAAAGTGTGTAAAGAGGGGGACAGAGAAATATCTATAAAGGCCATG 51  
 QY 879 TTACTCA 885  
 Db 50 TTACTCA 44

RESULT 4  
 AA625895/c.  
 LOCUS  
 DEFINITION  
 zulfat10.s1 Soares testis\_NHT Homo sapiens cDNA clone IMAGE:744954  
 3' mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 475)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin  
 J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B.,  
 White, X., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-NCI human EST Project

TITLE



Query Match 37.1% Score 624.8; DB 6; Length 3080;  
Best Local Similarity 76.5%; Pred No. 56-140;  
Matches 1000; Conservative 0; Mismatches 232; Indels 76; Gaps 16;

QY 2 TGGCAATCCGCCACTTACACACAACTCTTCTGCAGTTGCTCCAGCAATTAATTCGGAA 61  
DB TGGCCATCCGCCGCTTACGCACAACTCTTCTGCAGTTGCTCCAGCAATTAATTCGGAA 1527

QY 62 TGGGACCTGAGACTATACCAATTCAGGGTTACAGAGTGGATGAGAAACAACTAAGAGTGT 121  
DB TGGGACCTGAGACTATACCAATTCAGGGTTACAGAGTGGATGAGAAACAACTAAGAGTGT 1584

QY 122 CTATTCATTTGTTAAACCGACAGACATTCCTCCATCAGGCAATTTATTAACATTAATTCGA 181  
DB GTATTCATTTGTTAAACCGACAGACATTCCTCCATCAGGCAATTTATTAACATTAATTCGA 1644

QY 182 CCACATTAAGTCTCTAGTGAAGAAACCTTCTTGGGCAAGTAAGAAAGAGAGAACTACT 240  
DB CCACATTAAGTCTCTAGTGAAGAAACCTTCTTGGGCAAGTAAGAAAGAGAGAACTACT 1704

QY 241 CCAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB CCAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1764

QY 301 TGGGAGGATAGCTCGAAATTCAGGCTTAAACAAAGAGAGAGCAAAATTCCTTTCAGAT 360  
DB TGGAGGATAGCTCGAAATTCAGGCTTAAACAAAGAGAGAGCAAAATTCCTTTCAGAT 1824

QY 361 CTGCAATTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB CTGCAATTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884

QY 421 TATCAGACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB TATCAGACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1944

QY 481 ACTGAGAACCAATTTTGGTCTGCACTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538  
DB ACTGAGAACCAATTTTGGTCTGCACTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2004

QY 539 CTGCGACAGAGTGTGATATCCAGAGAGAGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 598  
DB CTGCGACAGAGTGTGATATCCAGAGAGAGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2064

QY 599 TGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658  
DB TGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124

QY 659 ATGTTTCAAAGGAGATTTGAACAAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718  
DB ATGTTTCAAAGGAGATTTGAACAAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2183

QY 719 GTCCACCGATGCTATTTCAAGACATATCCAGTGAATTAACAGTGAATGCTGCTGCTGCTGCT 778  
DB GTCCACCGATGCTATTTCAAGACATATCCAGTGAATTAACAGTGAATGCTGCTGCTGCTGCT 2241

QY 779 ATGATCTGATTTTACTGTTAGGAGATTTGATATTTTAAGTTA-CCATGATTAAGTGT 837  
DB ATGATCTGATTTTACTGTTAGGAGATTTGATATTTTAAGTTA-CCATGATTAAGTGT 2301

QY 838 GTAAAAAGGGGACAGAGAGAAATATATAAAGGCGCATGTTACTCATGCTGCTGCTGCTGCT 897  
DB GTAAAAAGGGGACAGAGAGAAATATATAAAGGCGCATGTTACTCATGCTGCTGCTGCTGCT 2346

QY 898 TGTGTGTTTCTGTAATAAGTGTACATTTATTTTATGAGTGGTTCCTGCTGCTGCTGCTGCTGCT 957  
DB TGTGTGTTTCTGTAATAAGTGTACATTTATTTTATGAGTGGTTCCTGCTGCTGCTGCTGCTGCT 2404

QY 958 ATAAAAATTAGGATCAGTTGAGAAATTTGAGAAATCAGATCAGTAAAGAACTGTT 1017  
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QY 1018 TGCTTTACCTGAATTTAACTATGAAACACACTT--AACAACTTACACGTTTCTAGATA 1075  
DB TCCTTTACCTGAATTTAACTATGAAACACACTT--AACAACTTACACGTTTCTAGATA 2494

QY 1076 TTAAGTGA-ATATGTAACCTCTCTCCATGGTATGATGTTATCTTTGA-CTTCTGTAAT 1133  
DB TTAAGTGA-ATATGTAACCTCTCTCCATGGTATGATGTTATCTTTGA-CTTCTGTAAT 2554

QY 1134 ATTTTGTATTTCTATCAGTGTATTAAGACATCTCTGGCTCCCTCGAGATCTTCTTAAGAA 1193  
DB ATTTTGTATTTCTATCAGTGTATTAAGACATCTCTGGCTCCCTCGAGATCTTCTTAAGAA 2603

QY 1194 CCACATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250  
DB CCACATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2663

QY 1251 GCATTTGTTAGTTTCCATGATTTAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1298  
DB GCATTTGTTAGTTTCCATGATTTAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2710

## RESULT 5

AB029065  
LOCUS  
DEFINITION  
Mus musculus Kkm mRNA for Ser/Thr kinase KKIAMRE-beta, complete cds.  
AB029065  
VERSION  
AB029065.1 GI:6594323  
KEYWORDS  
Ser/Thr kinase KKIAMRE-beta.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 4022)  
Sassa, T., Gomi, H., Sun, W., Ikeda, T., Thompson, R.P., and Itohara, S.  
The Murine KKIAMRE gene: variants, dual promoters, expression and chromosomal localization  
Unpublished  
JOURNAL  
2 (bases 1 to 4022)  
Sassa, T., Gomi, H. and Itohara, S.  
Direct Submission  
Submitted (16-JUN-1999) Takayuki Sassa, The Institute of Physical and Chemical Research (RIKEN), Brain Science Institute (BSI); 2-1 Hirotsawa, Wako, Saitama 351-0198, Japan  
E-mail: tsassa@brain.riken.go.jp, Tel: 81-48-467-9724 (ex. 7716), Fax: 81-48-467-9725  
FEATURES  
Location/Qualifiers  
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/organism="Mus musculus"  
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/tissue\_type="brain"  
/dev\_stage="adult"  
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1..4022  
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/protein\_id="BA08427.1"  
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